

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	FORSBERG, ET AL.	§	Docket No.: P02188US0
Serial No.:	NOT YET ASSIGNED	§	Examiner:
Filing Date:	07/06/2001	§	Art Unit:
Title:	A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY	§	
		§	
		§	
		§	

Box Sequence Listing  
 Assistant Commissioner for Patents  
 Washington, D.C. 20231

SEQUENCE LISTING 37 CFR 1.821

Dear Sir:

In compliance with 37 CFR 1.821, Applicants submit the attached sequence listing and provide one enclosed 3.5 inch disk. The file is stored as Seq.txt.

I hereby state that the content of the paper and computer readable copies of the sequence listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same.

Applicant believes that there is no additional fee required to file this paper. If Applicant is in error, the Commissioner is hereby authorized to charge any required fees and/or credits by this paper and during the entire pendency of this application to Account No. 06-2375/10104199.

July 6, 2001

Respectfully submitted,



Melissa W. Acosta, Ph.D.  
 Registration No. 45,872  
 FULBRIGHT & JAWORSKI L.L.P.  
 1301 McKinney, Suite 5100  
 Houston, Texas 77010-3095  
 (713) 651-5407 (Telephone)  
 (713) 651-5246 (Facsimile)

SEQUENCE LISTING

<110> FORSBERG, GORAN  
ERLANDSSON, EVA  
ANTONSSON, PER  
WALSE, BJORN

<120> A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

<130> P02188US0;10104199

<140> TBA

<141> 2001-06-20

<160> 7

<170> PatentIn version 3.0

<210> 1

<211> 672

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(672)

<223> Conjugate protein

<400> 1

Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr  
20 25 30

Tyr Met His Trp Val Lys Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe  
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr  
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val  
115 120 125

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr  
130 135 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr  
145 150 155 160

400400400400400400

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175  
 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser  
 180 185 190  
 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala  
 195 200 205  
 Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Ser Gly Gly  
 210 215 220  
 Pro Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys  
 225 230 235 240  
 Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr  
 245 250 255  
 Tyr Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe  
 260 265 270  
 Leu Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp  
 275 280 285  
 Tyr Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu  
 290 295 300  
 Tyr Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln  
 305 310 315 320  
 Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val  
 325 330 335  
 Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile  
 340 345 350  
 Asn Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val  
 355 360 365  
 Lys Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala  
 370 375 380  
 Arg His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe  
 385 390 395 400  
 Gly Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly  
 405 410 415  
 Ser Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp  
 420 425 430  
 Thr Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser  
 435 440 445  
 Leu Ser Ile Ser Leu Tyr Leu Tyr Thr Thr Ser Ile Val Met Thr Gln  
 450 455 460  
 Thr Pro Thr Ser Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr  
 465 470 475 480  
 Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Thr Ser Ser Arg  
500 505 510

Tyr Ala Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp  
515 520 525

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Ala Ala Val Tyr  
530 535 540

Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Thr  
545 550 555 560

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe  
565 570 575

Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys  
580 585 590

Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile  
595 600 605

Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln  
610 615 620

Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr  
625 630 635 640

Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His  
645 650 655

Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Ser  
660 665 670

<210> 2

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<221> Peptide

<222> (1)..(233)

<223> Chimeric Protein

<400> 2

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser  
1 5 10 15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr  
20 25 30

Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe Leu  
35 40 45

Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr  
50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu Tyr

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr  
 100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn  
115 120 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys  
130 135 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg  
145 150 155 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly  
165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser  
180 185 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr  
195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser Leu  
210 215 220

Ser Ile Ser Leu Tyr Leu Tyr Thr Thr  
225 230

<210> 3  
<211> 233  
<212> PRT  
<213> Artificial Sequence

```
<220>
<221> peptide
<222> (1)..(233)
<223> Chimeric Protein
```

<400> 3

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser  
1 5 10 15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr  
20 25 30

Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu  
35 40 45

Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr  
 50 55 60

Asn	Asp	Leu	Leu	Val	Asp	Leu	Gly	Ser	Lys	Asp	Ala	Thr	Asn	Lys	Tyr
65					70					75					80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys

85

90

95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr  
 100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn  
 115 120 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys  
 130 135 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg  
 145 150 155 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly  
 165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser  
 180 185 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr  
 195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu  
 210 215 220

His Ile Ala Leu Tyr Leu Tyr Thr Thr  
 225 230

<210> 4  
 <211> 233  
 <212> PRT  
 <213> *Staphylococcus* sp.

<400> 4

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser  
 1 5 10 15

Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr  
 20 25 30

Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu  
 35 40 45

Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp His Ser Trp Tyr  
 50 55 60

Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr  
 65 70 75 80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys  
 85 90 95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr  
 100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn  
 115 120 125

Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys

130

135

140

Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg  
 145 150 155 160

Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp  
 165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro  
 180 185 190

Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gln Tyr Ser Asn Thr  
 195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met  
 210 215 220

His Ile Asp Ile Tyr Leu Tyr Thr Ser  
 225 230

<210> 5

<211> 203

<212> PRT

<213> *Staphylococcus* sp.

<400> 5

Ala Leu His Lys Lys Ser Glu Leu Ser Ser Thr Ala Leu Asn Asn Met  
 1 5 10 15

Lys His Ser Tyr Ala Asp Ala Asn Pro Ile Ile Gly Ala Asn Lys Ser  
 20 25 30

Thr Gly Asp Gln Phe Leu Glu Asn Thr Leu Leu Tyr Lys Ala Phe Phe  
 35 40 45

Leu Leu Ile Asn Phe Asn Ser Ala Glu Met Ala Gln His Phe Lys Ser  
 50 55 60

Lys Asn Val Asp Val Tyr Ala Ile Arg Tyr Ala Ala Ala Cys Arg Thr  
 65 70 75 80

Ala Cys Thr Tyr Gly Gly Val Thr Pro His Ala Gly Asn Ala Leu Lys  
 85 90 95

Ala Arg Lys Ile Pro Ile Asn Leu Trp Ile Ile Gly Val Gln Lys  
 100 105 110

Glu Val Ser Leu Asp Lys Val Gln Thr Asp Lys Lys Asn Val Thr Val  
 115 120 125

Gln Glu Leu Asp Ala Gln Ala Arg Arg Tyr Leu Gln Lys Asp Leu Lys  
 130 135 140

Leu Tyr Asn Ala Ile Gln Arg Gly Lys Leu Glu Phe Asp Ser Ala Ala  
 145 150 155 160

Ala Ser Lys Val Ser Tyr Asp Leu Phe Asp Val Ala Gly Asp Phe Pro  
 165 170 175

Glu Lys Gln Leu Arg Ile Tyr Ser Asp Asn Lys Thr Leu Ser Thr Glu

T03010-93<0069601

0660

180

185

190

His Leu His Ile Asp Ile Tyr Leu Tyr Glu Ala  
195 200

<210> 6  
<211> 217  
<212> PRT  
<213> *Staphylococcus* sp.

<400> 6

Glu Asp Leu His Asp Lys Ser Glu Leu Thr Asp Leu Ala Leu Ala Asn  
1 5 10 15

Ala Tyr Gly Gln Tyr Asn His Pro Phe Ile Lys Glu Asn Ile Lys Ser  
                  20                 25                 30

Asp Glu Ile Ser Gly Glu Lys Asp Leu Ile Phe Arg Asn Gln Gly Asp  
35 40 45

Ser Gly Asn Asp Leu Arg Val Lys Phe Ala Thr Ala Asp Leu Ala Gln  
50 55 60

Lys Phe Lys Asn Lys Asn Val Asp Ile Tyr Gly Ala Ser Phe Tyr Tyr  
65 70 75 80

Lys Cys Glu Lys Ile Ser Glu Asn Ile Ser Glu Cys Leu Tyr Gly Gly  
85 90 95

Thr Thr Leu Asn Ser Glu Lys Leu Ala Gln Glu Arg Val Ile Gly Ala  
100 105 110

Asn Val Trp Val Asp Gly Ile Gln Lys Glu Thr Glu Leu Ile Arg Thr  
115 120 125

Asn Lys Lys Asn Val Thr Leu Gln Glu Leu Asp Ile Lys Ile Arg Lys  
 130 135 140

Ile Leu Ser Asp Lys Tyr Lys Ile Tyr Tyr Lys Asp Ser Glu Ile Ser  
 145 150 155 160

Lys Gly Leu Ile Glu Phe Asp Met Lys Thr Pro Arg Asp Tyr Ser Phe  
 165 170 175

Asp Ile Tyr Asp Leu Lys Gly Glu Asn Asp Tyr Glu Ile Asp Lys Ile  
180 185 190

Tyr Glu Asp Asn Lys Thr Leu Lys Ser Asp Asp Asp Ile Ser His Ile Asp  
195 200 205

Val Asn Leu Tyr Thr Lys Lys Lys Val  
210 215

<210> 7  
<211> 233  
<212> 227

<213> *Staphylococcus* sp.

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser  
 1 5 10 15  
 Glu Leu Gln Arg Asn Ala Leu Ser Asn Leu Arg Gln Ile Tyr Tyr Tyr  
 20 25 30  
 Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu  
 35 40 45  
 Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr  
 50 55 60  
 Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr  
 65 70 75 80  
 Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys  
 85 90 95  
 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr  
 100 105 110  
 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn  
 115 120 125  
 Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys  
 130 135 140  
 Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg  
 145 150 155 160  
 His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly  
 165 170 175  
 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser  
 180 185 190  
 Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gln Tyr Pro Asp Thr  
 195 200 205  
 Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu  
 210 215 220  
 His Ile Asp Leu Tyr Leu Tyr Thr Thr  
 225 230

0109010755, 0279501